0340/0540

#3

OIPE

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/967,305

DATE: 03/06/2002
TIME: 13:37:22

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\03062002\I967305.raw**

```
 4 <110> APPLICANT: Richardson, Jennifer
 5        Monahan, John
 7 <120> TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
 8        REFRACTORY AND METASTATIC PROSTATE CANCERS
10 <130> FILE REFERENCE: 07334-312001
12 <140> CURRENT APPLICATION NUMBER: US 09/967,305
13 <141> CURRENT FILING DATE: 2001-09-28
15 <150> PRIOR APPLICATION NUMBER: US 60/236,238
16 <151> PRIOR FILING DATE: 2000-09-28
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2005
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
28 ttgcaggctg ctgggctggg gctaagggct gctcagtttc cttcagcggg gcactgggaa      60
29 gcgccatggc actgcagggc atctcggtcg tggagctgtc cggcctggcc ccgggccccgt     120
30 tctgtgctat ggtcctggct gacttcgggg cgcgtgtggt acgcgtggac cggcccggct     180
31 cccgctacga cgtgagccgc ttgggccggg gcaagcgctc gctagtgctg gacctgaagc     240
32 agccgcgggg agccgccgtg ctgcggcgtc tgtgcaagcg gtcggatgtg ctgctggagc     300
33 ccttccgccg cggtgtcatg gagaaactcc agctgggccc agagattctg cagcgggaaa     360
34 atccaaggct tatttatgcc aggctgagtg gatttggcca gtcaggaagc ttctgccggt     420
35 tagctggcca cgatatcaac tatttggctt tgtcaggtgt tctctcaaaa attggcagaa     480
36 gtggtgagaa tccgtatgcc ccgctgaatc tcctggctga ctttgctggt ggtggcctta     540
37 tgtgtgcact gggcattata atggctcttt ttgaccgcac acgcactggc aagggtcagg     600
38 tcattgatgc aaatatggtg gaaggaacag catatttaag ttcttttctg tggaaaactc     660
39 agaaatcgag tctgtgggaa gcacctcgag gacagaacat gttggatggt ggagcacctt     720
40 tctatacgac ttacaggaca gcagatgggg aattcatggc tgttggagca atagaacccc     780
41 agttctacga gctgctgatc aaaggacttg gactaaagtc tgatgaactt cccaatcaga     840
42 tgagcatgga tgattggcca gaaatgaaga agaagtttgc agatgtattt gcaaagaaga     900
43 cgaaggcaga gtggtgtcaa atctttgacg gcacagatgc ctgtgtgact ccggttctga     960
44 cttttgagga ggttgttcat catgatcaca acaaggaacg gggctcgttt atcaccagtg    1020
45 aggagcagga cgtgagcccc cgccctgcac ctctgctgtt aaacacccca gccatccctt    1080
46 ctttcaaaag ggatcctttc ataggagaac acactgagga gatacttgaa gaatttggat    1140
47 tcagccgcga agagatttat cagcttaact cagataaaat cattgaaagt aataaggtaa    1200
48 aagctagtct ctaacttcca ggcccacggc tcaagtgaat ttgaatactg catttacagt    1260
49 gtagagtaac acataacatt gtatgcatgg aaacatggag gaacagtatt acagtgtcct    1320
50 accactctaa tcaagaaaag aattacagac tctgattcta cagtgatgat tgaattctaa    1380
51 aaatggttat cattagggct tttgatttat aaaactttgg gtacttatac taaattatgg    1440
52 tagttattct gccttccagt ttgcttgata tatttgttga tattaagatt cttgacttat    1500
53 attttgaatg ggttctagtg aaaaaggaat gatatattct tgaagacatc gatatacatt    1560
54 tatttacact cttgattcta caatgtagaa aatgaggaaa tgccacaaat tgtatggtga    1620
```

RAW SEQUENCE LISTING   DATE: 03/06/2002
PATENT APPLICATION: US/09/967,305   TIME: 13:37:22

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\03062002\I967305.raw**

```
55 taaaagtcac gtgaaacaga gtgattggtt gcatccaggc cttttgtctt ggtgttcatg   1680
56 atctccctct aagcacattc caaactttag caacagttat cacactttgt aatttgcaaa   1740
57 gaaaagtttc acctgtattg aatcagaatg ccttcaactg aaaaaaacat atccaaaata   1800
58 atgaggaaat gtgttggctc actacgtaga gtccagaggg acagtcagtt ttagggttgc   1860
59 ctgtatccag taactcgggg cctgtttccc cgtgggtctc tgggctgtca gctttccttt   1920
60 ctccatgtgt ttgatttctc ctcaggctgg tagcaagttc tggatcttat acccaacaca   1980
61 cagcaacatc cagaaataaa gttct                                          2005
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 382
65 <212> TYPE: PRT
66 <213> ORGANISM: Homo sapiens
68 <400> SEQUENCE: 2
69 Met Ala Leu Gln Gly Ile Ser Val Val Glu Leu Ser Gly Leu Ala Pro
70  1               5                   10                  15
71 Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
72           .20                  25                  30
73 Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
74           35                  40                  45
75 Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
76       50                  55                  60
77 Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
78  65                  70                  75                  80
79 Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
80                   85                  90                  95
81 Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
82               100                 105                 110
83 Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
84           115                 120          .        125
85 Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
86       130                 135                 140
87 Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
88 145                 150                 155                 160
89 Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Gly Lys
90               165                 170                 175
91 Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
92           180                 185                 190
93 Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
94           195                 200                 205
95 Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
96       210                 215                 220
97 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
98 225                 .   230                 235                 240
99 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
100                 245                 250                 255
101 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
102             260                 265 ·               270
103 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
104         275                 280                 285
105 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
```

```
106     290                    295                    300
107 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
108 305                    310                    315                    320
109 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
110                    325                    330                    335
111 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
112                    340                    345                    350
113 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
114            355                    360                    365
115 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
116     370                    375                    380
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 1146
120 <212> TYPE: DNA
121 <213> ORGANISM: Homo sapiens
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (1)...(1146)
127 <400> SEQUENCE: 3
128 atg gca ctg cag ggc atc tcg gtc gtg gag ctg tcc ggc ctg gcc ccg      48
129 Met Ala Leu Gln Gly Ile Ser Val Val Glu Leu Ser Gly Leu Ala Pro
130   1             5               10                  15
132 ggc ccg ttc tgt gct atg gtc ctg gct gac ttc ggg gcg cgt gtg gta      96
133 Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
134             20              25                  30
136 cgc gtg gac cgg ccc ggc tcc cgc tac gac gtg agc cgc ttg ggc cgg     144
137 Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
138             35              40                  45
140 ggc aag cgc tcg cta gtg ctg gac ctg aag cag ccg cgg gga gcc gcc     192
141 Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
142        50                  55                  60
144 gtg ctg cgg cgt ctg tgc aag cgg tcg gat gtg ctg ctg gag ccc ttc     240
145 Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
146  65                  70                  75                  80
148 cgc cgc ggt gtc atg gag aaa ctc cag ctg ggc cca gag att ctg cag     288
149 Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
150                  85                  90                  95
152 cgg gaa aat cca agg ctt att tat gcc agg ctg agt gga ttt ggc cag     336
153 Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
154            100                 105                 110
156 tca gga agc ttc tgc cgg tta gct ggc cac gat atc aac tat ttg gct     384
157 Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
158            115                 120                 125
160 ttg tca ggt gtt ctc tca aaa att ggc aga agt ggt gag aat ccg tat     432
161 Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
162        130                 135                 140
164 gcc ccg ctg aat ctc ctg gct gac ttt gct ggt ggt ggc ctt atg tgt     480
165 Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
166 145                 150                 155                 160
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/967,305
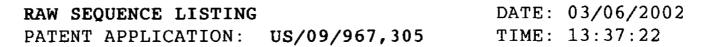
DATE: 03/06/2002
TIME: 13:37:22

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\03062002\I967305.raw**

```
168 gca ctg ggc att ata atg gct ctt ttt gac cgc aca cgc act ggc aag      528
169 Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Gly Lys
170              165             170             175
172 ggt cag gtc att gat gca aat atg gtg gaa gga aca gca tat tta agt      576
173 Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
174              180             185             190
176 tct ttt ctg tgg aaa act cag aaa tcg agt ctg tgg gaa gca cct cga      624
177 Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
178              195             200             205
180 gga cag aac atg ttg gat ggt gga gca cct ttc tat acg act tac agg      672
181 Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
182     210             215             220
184 aca gca gat ggg gaa ttc atg gct gtt gga gca ata gaa ccc cag ttc      720
185 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
186 225             230             235             240
188 tac gag ctg ctg atc aaa gga ctt gga cta aag tct gat gaa ctt ccc      768
189 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
190              245             250             255
192 aat cag atg agc atg gat gat tgg cca gaa atg aag aag aag ttt gca      816
193 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
194              260             265             270
196 gat gta ttt gca aag aag acg aag gca gag tgg tgt caa atc ttt gac      864
197 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
198              275             280             285
200 ggc aca gat gcc tgt gtg act ccg gtt ctg act ttt gag gag gtt gtt      912
201 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
202     290             295             300
204 cat cat gat cac aac aag gaa cgg ggc tcg ttt atc acc agt gag gag      960
205 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
206 305             310             315             320
208 cag gac gtg agc ccc cgc cct gca cct ctg ctg tta aac acc cca gcc     1008
209 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
210              325             330             335
212 atc cct tct ttc aaa agg gat cct ttc ata gga gaa cac act gag gag     1056
213 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
214              340             345             350
216 ata ctt gaa gaa ttt gga ttc agc cgc gaa gag att tat cag ctt aac     1104
217 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
218              355             360             365
220 tca gat aaa atc att gaa agt aat aag gta aaa gct agt ctc             1146
221 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
222     370             375             380
224 <210> SEQ ID NO: 4
225 <211> LENGTH: 2069
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (90)...(1235)
```

```
RAW SEQUENCE LISTING              DATE: 03/06/2002
PATENT APPLICATION:  US/09/967,305   TIME: 13:37:22

           Input Set : A:\SEQUENCE LISTING.txt
           Output Set: N:\CRF3\03062002\I967305.raw


233 <400> SEQUENCE: 4
234 gggcgccggg attgggaggg cttcttgcag gctgctgggc tggggctaag ggctgctcag      60
235 tttccttcag cggggcactg ggaagcgcc atg gca ctg cag ggc atc tcg gtc        113
236                                 Met Ala Leu Gln Gly Ile Ser Val
237                                  1               5
239 gtg gag ctg tcc ggc ctg gcc ccg ggc ccg ttc tgt gct atg gtc ctg       161
240 Val Glu Leu Ser Gly Leu Ala Pro Gly Pro Phe Cys Ala Met Val Leu
241       10                  15                  20
243 gct gac ttc ggg gcg cgt gtg gta cgc gtg gac cgg ccc ggc tcc cgc       209
244 Ala Asp Phe Gly Ala Arg Val Val Arg Val Asp Arg Pro Gly Ser Arg
245 25                  30                  35                  40
247 tac gac gtg agc cgc ttg ggc cgg ggc aag cgc tcg cta gtg ctg gac       257
248 Tyr Asp Val Ser Arg Leu Gly Arg Gly Lys Arg Ser Leu Val Leu Asp
249                  45                  50                  55
251 ctg aag cag ccg cgg gga gcc gcc gtg ctg cgg cgt ctg tgc aag cgg       305
252 Leu Lys Gln Pro Arg Gly Ala Ala Val Leu Arg Arg Leu Cys Lys Arg
253                  60                  65                  70
255 tcg gat gtg ctg ctg gag ccc ttc cgc cgc ggt gtc atg gag aaa ctc       353
256 Ser Asp Val Leu Leu Glu Pro Phe Arg Arg Gly Val Met Glu Lys Leu
257             75                  80                  85
259 cag ctg ggc cca gag att ctg cag cgg gaa aat cca agg ctt att tat       401
260 Gln Leu Gly Pro Glu Ile Leu Gln Arg Glu Asn Pro Arg Leu Ile Tyr
261       90                  95                 100
263 gcc agg ctg agt gga ttt ggc cag tca gga agc ttc tgc cgg tta gct       449
264 Ala Arg Leu Ser Gly Phe Gly Gln Ser Gly Ser Phe Cys Arg Leu Ala
265 105                 110                 115                 120
267 ggc cac gat atc aac tat ttg gct ttg tca ggt gtt ctc tca aaa att       497
268 Gly His Asp Ile Asn Tyr Leu Ala Leu Ser Gly Val Leu Ser Lys Ile
269                 125                 130                 135
271 ggc aga agt ggt gag aat ccg tat gcc ccg ctg aat ctc ctg gct gac       545
272 Gly Arg Ser Gly Glu Asn Pro Tyr Ala Pro Leu Asn Leu Leu Ala Asp
273                 140                 145                 150
275 ttt gct ggt ggt ggc ctt atg tgt gca ctg ggc att ata atg gct ctt       593
276 Phe Ala Gly Gly Gly Leu Met Cys Ala Leu Gly Ile Ile Met Ala Leu
277             155                 160                 165
279 ttt gac cgc aca cgc act ggc aag ggt cag gtc att gat gca aat atg       641
280 Phe Asp Arg Thr Arg Thr Gly Lys Gly Gln Val Ile Asp Ala Asn Met
281       170                 175                 180
283 gtg gaa gga aca gca tat tta agt tct ttt ctg tgg aaa act cag aaa       689
284 Val Glu Gly Thr Ala Tyr Leu Ser Ser Phe Leu Trp Lys Thr Gln Lys
285 185                 190                 195                 200
287 tcg agt ctg tgg gaa gca cct cga gga cag aac atg ttg gat ggt gga       737
288 Ser Ser Leu Trp Glu Ala Pro Arg Gly Gln Asn Met Leu Asp Gly Gly
289                 205                 210                 215
291 gca cct ttc tat acg act tac agg aca gca gat ggg gaa ttc atg gct       785
292 Ala Pro Phe Tyr Thr Thr Tyr Arg Thr Ala Asp Gly Glu Phe Met Ala
293                 220                 225                 230
295 gtt gga gca ata gaa ccc cag ttc tac gag ctg ctg atc aaa gga ctt       833
296 Val Gly Ala Ile Glu Pro Gln Phe Tyr Glu Leu Leu Ile Lys Gly Leu
```

VERIFICATION SUMMARY   DATE: 03/06/2002
PATENT APPLICATION: US/09/967,305   TIME: 13:37:23

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\03062002\I967305.raw**